OIPE 02Co

## CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/441,857

CRF Processing Date: 12/9/99
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: ENTERED

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☑ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: 25

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

_____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

**RAW SEQUENCE LISTING**
PATENT APPLICATION **US/09/441,857**

DATE: 12/10/1999
TIME: 10:09:05

Input Set: **I441857.RAW**

**This Raw Listing contains the General Information Section and up to first 5 pages.**

<110> APPLICANT: Duffy, Hao-Peng Xu
Shan, Ji-dong
Yuan, Li-ming
Dudman, Daniel
Calabro, Anthony
<120> TITLE OF INVENTION: Identification of Differentially Methylated Multiple Drug Resistance Loci
<130> FILE REFERENCE: 52494/2202
<140> CURRENT APPLICATION NUMBER: US/09/441,857
<141> CURRENT FILING DATE: 1999-11-18
<150> EARLIER APPLICATION NUMBER: US 60/108,994
<151> EARLIER FILING DATE: 1998-11-08
<160> NUMBER OF SEQ ID NOS: 46
<170> SOFTWARE: WordPerfect 8.0 for Windows
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic adapter
<400> SEQUENCE: 1
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<211> LENGTH: 12
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic adapter
<400> SEQUENCE: 2
cggtgaagca ct 12
<210> SEQ ID NO 3
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic adapter
<400> SEQUENCE: 3
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<211> LENGTH: 12
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic adapter

<400> SEQUENCE: 4
cggactacag ca 12

<210> SEQ ID NO 5
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic adapter
<400> SEQUENCE: 5
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic adapter
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cggtctgaac ct 12

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: 48..573
<400> SEQUENCE: 7

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                                                    Met Ser Ala
                                                      1
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Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu Val Phe Leu
      5                  10                  15
ggg gag caa agc gtt gca aag aca tct ttg atc acc aga ttc agg tat     152
Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg Phe Arg Tyr
 20                  25                  30                  35
gac agt ttt gac aac acc tat cag gca ata att ggc att gac ttt tta     200
Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile Asp Phe Leu
                 40                  45                  50
tca aaa act atg tac ttg gag gat gga aca atc ggg ctt cgg ctg tgg     248
Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu Arg Leu Trp
             55                  60                  65
gat acg gcg ggt cag gaa cgt ctc cgt agc ctc att ccc agg tac atc     296
Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro Arg Tyr Ile
         70                  75                  80
cgt gat tct gct gca gct gta gta gtt tac gat atc aca aat gtt aac     344
Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr Asn Val Asn
     85                  90                  95
tca ttc cag caa act aca aag tgg att gat gat gtc aga aca gaa aga     392
Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg Thr Glu Arg
100                 105                 110                 115
```

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 95          gga agt gat gtt atc atc acg cta gta gga aat aga aca gat ctt gct     440
 96          Gly Ser Asp Val Ile Ile Thr Leu Val Gly Asn Arg Thr Asp Leu Ala
 97                       120                 125                 130
 98          gac aag agg caa gtg tca gtt gag gag gga gag agg aaa gcc aaa ggg     488
 99          Asp Lys Arg Gln Val Ser Val Glu Glu Gly Glu Arg Lys Ala Lys Gly
100                   135                 140                 145
101          ctg aat gtt acg ttt att gaa act agg gca aaa act gga tac aat gta     536
102          Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr Gly Tyr Asn Val
103                 150                 155                 160
104          aag cag ctc ttt cga cgt gta gca gca gct ttg ccg g                   573
105          Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro
106              165                 170                 175
107     <210> SEQ ID NO 8
108     <211> LENGTH: 23
109     <212> TYPE: DNA
110     <213> ORGANISM: Artificial Sequence
111     <220> FEATURE:
112     <223> OTHER INFORMATION: Synthetic primer
113     <400> SEQUENCE: 8
114          tcctctagtt ccaccatgtc cac                                           23
115     <210> SEQ ID NO 9
116     <211> LENGTH: 19
117     <212> TYPE: DNA
118     <213> ORGANISM: Artificial Sequence
119     <220> FEATURE:
120     <223> OTHER INFORMATION: Synthetic primer
121     <400> SEQUENCE: 9
122          cacagccgaa gcccgattg                                                 19
123     <210> SEQ ID NO 10
124     <211> LENGTH: 838
125     <212> TYPE: DNA
126     <213> ORGANISM: Homo sapiens
127     <220> FEATURE:
128     <221> NAME/KEY: CDS
129     <222> LOCATION: 48..809
130     <400> SEQUENCE: 10
131          ccgggaggtc tctgggctga ggcggcgaca gctcctctag ttccacc atg tcc gcg      56
132                                                          Met Ser Ala
133                                                            1
134          ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg gtg ttc ctg     104
135          Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu Val Phe Leu
136                5                  10                  15
137          ggg gag caa agc gtt gca aag aca tct ttg atc acc aga ttc agg tat     152
138          Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg Phe Arg Tyr
139           20                  25                  30                  35
140          gac agt ttt gac aac acc tat cag gca ata att ggc att gac ttt tta     200
141          Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile Asp Phe Leu
142                           40                  45                  50
143          tca aaa act atg tac ttg gag gat gga aca atc ggg ctt cgg ctg tgg     248
144          Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu Arg Leu Trp
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```
                    55                  60                  65
gat acg gcg ggt cag gaa cgt ctc cgt agc ctc att ccc agg tac atc     296
Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro Arg Tyr Ile
          70                  75                  80
cgt gat tct gct gca gct gta gta gtt tac gat atc aca aat gtt aac     344
Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr Asn Val Asn
     85                  90                  95
tca ttc cag caa act aca aag tgg att gat gat gtc aga aca gaa aga     392
Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg Thr Glu Arg
100                 105                 110                 115
gga agt gat gtt atc atc acg cta gta gga aat aga aca gat ctt gct     440
Gly Ser Asp Val Ile Ile Thr Leu Val Gly Asn Arg Thr Asp Leu Ala
                120                 125                 130
gac aag agg caa gtg tca gtt gag gag gga gag agg aaa gcc aaa ggg     488
Asp Lys Arg Gln Val Ser Val Glu Glu Gly Glu Arg Lys Ala Lys Gly
            135                 140                 145
ctg aat gtt acg ttt att gaa act agg gca aaa act gga tac aat gta     536
Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr Gly Tyr Asn Val
        150                 155                 160
aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga atg gaa agc     584
Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly Met Glu Ser
    165                 170                 175
aca cag gac gga agc aga gaa gac atg agt gac ata aaa ctg gaa aag     632
Thr Gln Asp Gly Ser Arg Glu Asp Met Ser Asp Ile Lys Leu Glu Lys
180                 185                 190                 195
cct cag gag caa aca gtc agc gaa ggg ggt tgt tcc tgc tac tct ccc     680
Pro Gln Glu Gln Thr Val Ser Glu Gly Gly Cys Ser Cys Tyr Ser Pro
                200                 205                 210
atg tca tct tca acc ctt cct cag aag ccc cct tac tct ttc att gac     728
Met Ser Ser Ser Thr Leu Pro Gln Lys Pro Pro Tyr Ser Phe Ile Asp
            215                 220                 225
tgc agt gtg aat att ggc ttg aac ctt ttc cct tca tta ata acg ttt     776
Cys Ser Val Asn Ile Gly Leu Asn Leu Phe Pro Ser Leu Ile Thr Phe
        230                 235                 240
tgc aat tca tca ttg ctg cct gtc tcg tgg aga tgatctatta gcttgacaag   829
Cys Asn Ser Ser Leu Leu Pro Val Ser Trp Arg
    245                 250             254
cacaaaaaa                                                          838
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: 1..762
<400> SEQUENCE: 11
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Met Ser Ala Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu
  1               5                  10                  15
gtg ttc ctg ggg gag caa agc gtt gca aag aca tct ttg atc acc aga      96
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195         Val Phe Leu Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg
196                      20                  25                  30
197         ttc agg tat gac agt ttt gac aac acc tat cag gca ata att ggc att     144
198         Phe Arg Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile
199                  35                  40                  45
200         gac ttt tta tca aaa act atg tac ttg gag gat gga aca atc ggg ctt     192
201         Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu
202              50                  55                  60
203         cgg ctg tgg gat acg gcg ggt cag gaa cgt ctc cgt agc ctc att ccc     240
204         Arg Leu Trp Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro
205          65                  70                  75                  80
206         agg tac atc cgt gat tct gct gca gct gta gta gtt tac gat åtc aca     288
207         Arg Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr
208                          85                  90                  95
209         aat gtt aac tca ttc cag caa act aca aag tgg att gat gat gtc aga     336
210         Asn Val Asn Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg
211                      100                 105                 110
212         aca gaa aga gga agt gat gtt atc atc acg cta gta gga aat aga aca     384
213         Thr Glu Arg Gly Ser Asp Val Ile Ile Thr Leu Val Gly Asn Arg Thr
214                  115                 120                 125
215         gat ctt gct gac aag agg caa gtg tca gtt gag gag gga gag agg aaa     432
216         Asp Leu Ala Asp Lys Arg Gln Val Ser Val Glu Glu Gly Glu Arg Lys
217              130                 135                 140
218         gcc aaa ggg ctg aat gtt acg ttt att gaa act agg gca aaa act gga     480
219         Ala Lys Gly Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr Gly
220         145                 150                 155                 160
221         tac aat gta aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga     528
222         Tyr Asn Val Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly
223                          165                 170                 175
224         atg gaa agc aca cag gac gga agc aga gaa gac atg agt gac ata aaa     576
225         Met Glu Ser Thr Gln Asp Gly Ser Arg Glu Asp Met Ser Asp Ile Lys
226                      180                 185                 190
227         ctg gaa aag cct cag gag caa aca gtc agc gaa ggg ggt tgt tcc tgc     624
228         Leu Glu Lys Pro Gln Glu Gln Thr Val Ser Glu Gly Gly Cys Ser Cys
229                  195                 200                 205
230         tac tct ccc atg tca tct tca acc ctt cct cag aag ccc cct tac tct     672
231         Tyr Ser Pro Met Ser Ser Ser Thr Leu Pro Gln Lys Pro Pro Tyr Ser
232              210                 215                 220
233         ttc att gac tgc agt gtg aat att ggc ttg aac ctt ttc cct tca tta     720
234         Phe Ile Asp Cys Ser Val Asn Ile Gly Leu Asn Leu Phe Pro Ser Leu
235         225                 230                 235                 240
236         ata acg ttt tgc aat tca tca ttg ctg cct gtc tcg tgg aga             762
237         Ile Thr Phe Cys Asn Ser Ser Leu Leu Pro Val Ser Trp Arg
238                          245                 250                 254
239   <210> SEQ ID NO 12
240   <211> LENGTH: 254
241   <212> TYPE: PRT
242   <213> ORGANISM: Homo sapiens
243   <400> SEQUENCE: 12
244         Met Ser Ala Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu
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**VERIFICATION SUMMARY**
PATENT APPLICATION **US/09/441,857**

DATE: 12/10/1999
TIME: 10:09:05

Input Set: **I441857.RAW**

| Line | ? | Error/Warning | Original Text |
|---|---|---|---|

## PREVIOUSLY ERRORED SEQUENCES-EDITED

<210> 25
<211> 1460
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 420..1043
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<223> cDNA (composite of multiple cDNA clones)
<400> 25

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agggaacggc cctagctttg ggaagccaga ggacacccct ggctcctgcc gacaccgccc   180
tccttccctt cccagccgcg ggcctcgctc ggtgctaggc tactctgccg ggaggcggcg   240
gcggctgcca gtctgtggag agtcctgctg ccctccagcc gggctcctcc accgggcctt   300
gcaggggccg agagagctcg gtgcccgccc ttccgctcgc ctttttcgtc agctggctgg   360
agcagcatcg gtccgggagg tctctaggct gaggcggcgg ccgctcctct agttccaca    419
atg tcc acg ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg      467
Met Ser Thr Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu
  1               5                  10                  15
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             20                  25                  30
ttc atg tat gac agt ttt gac aac acc tat cag gca aca att ggc att      563
Phe Met Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile
         35                  40                  45
gac ttt tta tca aaa act atg tac ttg gag gat cga aca atc agg ctt      611
Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Arg Thr Ile Arg Leu
     50                  55                  60
cag ctg tgg gat act gcg ggt cag gaa cgt ttc cgt agc ctc att ccc      659
Gln Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro
 65                  70                  75                  80
agt tac atc cgt gat tct gct gca gct gta gta gtt tac gat atc aca      707
Ser Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr
                 85                  90                  95
aat gtt aac tca ttc cag caa act aca aag tgg att gat gat gtc aga      755
Asn Val Asn Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg
            100                 105                 110
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Thr Glu Arg Gly Ser Asp Val Ile Ile Met Leu Val Gly Asn Lys Thr
        115                 120                 125
gat ctt gct gac aag agg caa gtg tca att gag gag gga gag agg aaa      851
Asp Leu Ala Asp Lys Arg Gln Val Ser Ile Glu Glu Gly Glu Arg Lys
    130                 135                 140
gcc aaa gag ctg aat gtt atg ttt att gaa act agt gca aaa gct gga      899
Ala Lys Glu Leu Asn Val Met Phe Ile Glu Thr Ser Ala Lys Ala Gly
145                 150                 155                 160
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48          tac aat gta aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga     947
49          Tyr Asn Val Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly
50                      165                 170                 175
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51          atg gaa agc aca cag gac aga agc aga gaa gat atg att gac ata aaa     995
52          Met Glu Ser Thr Gln Asp Arg Ser Arg Glu Asp Met Ile Asp Ile Lys
53                      180                 185                 190
54          ctg gaa aag cct cag gag caa cca gtc agt gaa gga ggc tgt tcc tgc    1043
55          Leu Glu Lys Pro Gln Glu Gln Pro Val Ser Glu Gly Gly Cys Ser Cys
56                  195                 200                 205
57          taatctccca tgtcatcttc aaccttcttc agaagctcac tgctttggcc cccttactct  1103
58          ttcattgact gcagtgtgaa tattggcttg aacctttcc cttcagtaat aacgtattgc  1163
59          aattcatcat tgctgcctgt ctcgtggaga tgatctatta gcttcacaag cacaacaaaa  1223
60          gtcagtgtct tcattattta tattttacaa aaagccaaaa tatttcagca tattccagtg  1283
61          ataactttaa aaattagata cattttctta acatttttt ctttttaat gttatgataa  1343
62          tgtacttcaa aatgatggaa atctcaacag tatgagtatg gcttggttaa cgagcggtat  1403
63          gttcacagcc tactttatct ctccttgctt ttctcacctc tcacttaccc ggaattc     1460
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This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

<110> Duffy, Hao-Peng Xu
Shan, Ji-dong
Yuan, Li-ming
Dudman, Daniel
Calabro, Anthony
<120> Identification of Differentially Methylated Multiple Drug Resistance Loci
<130> 52494/2202
<140> US/09/441,857
<141> 1999-11-18
<150> US 60/108,994
<151> 1998-11-08
<160> 46
<170> WordPerfect 8.0 for Windows

## ERRORED SEQUENCES FOLLOW

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<210> 25
<211> 1460
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 420..1043
<220>
<223> cDNA (composite of multiple cDNA clones)
<400> 25

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ggttccggct ccgccaccct cagcttctct tccccaggtc tgggagccga gtgcggaagg 120
agggaacggc cctagctttg ggaagccaga ggacacccct ggctcctgcc gacaccgccc 180
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gcggctgcca gtctgtggag agtcctgctg ccctccagcc gggctcctcc accgggcctt 300
gcaggggccg agagagctcg gtgcccgccc ttccgctcgc ctttttcgtc agctggctgg 360
agcagcatcg gtccgggagg tctctaggct gaggcggcgg ccgctcctct agttccaca 419
atg tcc acg ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg 467
Met Ser Thr Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu
1 5 10 15
gtg ttc ctg ggg gag caa agc gtt gga aag aca tct ttg atc acc aga 515
Val Phe Leu Gly Glu Gln Ser Val Gly Lys Thr Ser Leu Ile Thr Arg
20 25 30
ttc atg tat gac agt ttt gac aac acc tat cag gca aca att ggc att 563
Phe Met Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile

```
40                  35                  40                  45
41          gac ttt tta tca aaa act atg tac ttg gag gat cga aca atc agg ctt     611
42          Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Arg Thr Ile Arg Leu
43               50                  55                  60
44          cag ctg tgg gat act gcg ggt cag gaa cgt ttc cgt agc ctc att ccc     659
45          Gln Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro
46           65                  70                  75                  80
47          agt tac atc cgt gat tct gct gca gct gta gta gtt tac gat atc aca     707
48          Ser Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr
49                          85                  90                  95
50          aat gtt aac tca ttc cag caa act aca aag tgg att gat gat gtc aga     755
51          Asn Val Asn Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg
52                      100                 105                 110
53          aca gaa aga gga agt gat gtt atc atc atg cta gta gga aat aaa aca     803
54          Thr Glu Arg Gly Ser Asp Val Ile Ile Met Leu Val Gly Asn Lys Thr
55                  115                 120                 125
56          gat ctt gct gac aag agg caa gtg tca att gag gag gga gag agg aaa     851
57          Asp Leu Ala Asp Lys Arg Gln Val Ser Ile Glu Glu Gly Glu Arg Lys
58              130                 135                 140
59          gcc aaa gag ctg aat gtt atg ttt att gaa act agt gca aaa gct gga     899
60          Ala Lys Glu Leu Asn Val Met Phe Ile Glu Thr Ser Ala Lys Ala Gly
61          145                 150                 155                 160
62          tac aat gta aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga     947
63          Tyr Asn Val Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly
64                          165                 170                 175
65          atg gaa agc aca cag gac aga agc aga gaa gat atg att gac ata aaa     995
66          Met Glu Ser Thr Gln Asp Arg Ser Arg Glu Asp Met Ile Asp Ile Lys
67                      180                 185                 190
68          ctg gaa aag cct cag gag caa cca gtc agt gaa gga ggc tgt tcc tgc    1043
69          Leu Glu Lys Pro Gln Glu Gln Pro Val Ser Glu Gly Gly Cys Ser Cys
70                  195                 200                 205
71          taatctccca tgtcatcttc aaccttcttc agaagctcac tgctttggcc cccttactct  1103
72          ttcattgact gcagtgtgaa tattggcttg aacctttcc cttcagtaat aacgtattgc  1163
73          aattcatcat tgctgcctgt ctcgtggaga tgatctatta gcttcacaag cacaacaaaa  1223
74          gtcagtgtct tcattattta tattttacaa aaagccaaaa tatttcagca tattccagtg  1283
E-->  75  ataactttaa aaattagata cattttctta acatttttt ctttttaat gttatgataa  1243
76          tgtacttcaa aatgatggaa atctcaacag tatgagtatg gcttggttaa cgagcggtat  1403
77          gttcacagcc tactttatct ctccttgctt ttctcacctc tcacttaccc ggaattc     1460
```

1343

**VERIFICATION SUMMARY**
PATENT APPLICATION **US/09/441,857**

DATE: 12/09/1999
TIME: 15:11:06

Input Set: **I441857.RAW**

| Line | ? | Error/Warning | Original Text |
|---|---|---|---|
| 75 | E | Number of Bases conflict w/ Running Total | ataactttaa aaattagata cattttctta acattttt |